REMARKS

I. **Structure of this Response**

Section II provides basis for the amendment to the specification and refers to submission of a paper copy and computer readable copy of the Substitute Sequence Listing required in the *Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, 37 C.F.R. §§ 1.821-1.825* that accompanied the Office Action.

Section III provides a substitute specification, as required in the Office Action.

Section IV provides a response, with traverse, to the restriction requirement contained in the Office Action.

II. **Amendment to Specification**

Amendments to pages 7, 8, 9, 10, 11, 14, 15, 16, 18 and page 26, lines 21, 23, 24 and 28, page 27, lines 20 and 26, page 28, lines 28 and 29, page 42, page 43, lines 1, 2, 4, 6 and 7, pages 44 and 167, and page 178, line 2 were made to reflect changes in SEQ ID NO: numbering made necessary by the deletion of the sequences (*i.e.*, SEQ ID NOS:4-6 and SEQ ID NOS:114-116) which did not conform with the requirements of C.F.R. §§ 1.821-1.825, as correctly pointed out by the Office Action mailed September 26, 2000, and the accompanying "Raw Sequence Listing" error report.

Similarly, the amendments to page 27, line 30, and page 43, line 14, were made necessary by the inclusion of the peptide motif (SEQ ID NO:4) which was the subject of the Applicant's denied Petition to Waive the "Sequence Rules", as noted in the Office Action.

The amendment on page 36, lines 10 and 11, change the Figure number referring to the sequence for "clone 712562" containing the human EST in GenBank Accession No. AA281296 to conform to the reference to the same sequence found on page 156, lines 11 and 12, where Figure 59 is identified.

The amendment to page 46, line 28 corrects the description of the symbol used to identify similar amino acids in Figure 25 from a "circle (M)" to reflect the actual symbol used in the Figure.

The amendment on page 198, line 1, corrects an error of a typographical nature. Support for this amendment can be found on page 250 in parent application PCT/US97/17885, filed October 1, 1997, where the correct primer designation "hTR-445" appears.

Other amendments not referred to above were made to correct typographical and minor errors.

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-476, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

III. **Substitute Specification**

As required by the Office Action, applicants submit herewith a substitute specification reflecting the changes to the specification made by the amendments dated November 28, 1998, March 30, 1999, and those contained in this amendment.

Also enclosed is a marked-up version as required under 37 C.F.R. 1.125(b), showing changes implemented by the amendments made herein, i.e., compared to the specification of record.

The Substitute Specification includes no new matter.

IV. **Response to Restriction Requirement**

Applicants respectfully traverse in part the present restriction requirement. In Paper No. 9, Applicants responded to an 8-way restriction requirement by electing Group II. The Office has now required an additional 48-way restriction requirement. The reason for the restriction is stated to be "to maintain consistency between the present application and Applicant's copending applications . . ." Applicants respectfully urge this is not a proper basis for restriction. Following the reasoning of the Office, Applicants would be required to file and prosecute *at least* 48 different patent applications, at great expense.

Accordingly, Applicants reaffirm election of polynucleotide claims (previously Group II, now Groups 7-12). This election is made without traverse as to division between polynucleotide claims, other composition claims, and method claims. However, Applicants do traverse division between species of origin in Groups 7-12. Applicants provisionally elect Group 11, but believe that at least Groups 7-12 should be rejoined, for the reasons given below. In view of this provisional election and request for rejoinder, should a species requirement be imposed, Applicants provisionally elect vertebrate telomerase as the species for examination (Claim 105). Present claims 105-107 and 110 are believed to fall in the elected group.

With regard to the restriction requirement of Groups 7-12, Applicants respectfully submit that this restriction is improper. Different groups are being identified within a single claim, e.g., Claim 93. Like new claim 105, Claim 93 is directed to a nucleic acid identified, in part, by a strucural motif.

Applicants respectfully submit that decisions by the PTO Board of Appeals and its reviewing court establish that a restriction requirement which compels the Applicants to divide a single generic claim is improper; and that regardless of the language employed by the examiner such a procedure amounts to a rejection. See *Ex parte Holt,* 214 USPQ 381 (Bd. App. 1982), *In re Haas,* 179 USPQ 623 (CCPA 1973); *In re Haas,* 198 USPQ 334 (CCPA 1978); and *In re Weber,* 198 USPQ 331 (CCPA 1978). This premise was best summarized by the Court *In re Weber,* as follows:

> As a general proposition, an applicant has a right to have *each* claim examined on the merits. If a applicant submits a number of claims, it may well be that pursuant to a proper restriction requirement, those claims will be dispersed to a number of applications. Such action would not affect the right of the applicant eventually to have each of the claims examined in the form he considers to best define his invention. If, however, a single claim is required to be divided up and presented in several applications, that claim would never be considered on the merits. The totality of the resulting fragmentary claims would not necessarily be the equivalent of the original claim. Further, since the subgenera would be defined by the examiner rather than by the applicant, it is not inconceivable that a number of the fragments would not be described in the specification.

Thus, the PTO may not, prior to examining and properly rejecting a claim, use a restriction requirement to compel the excision of subject matter from the claim or permanently withdraw from consideration any subject matter which reads on the restricted claim. Furthermore, sequence data for all the TRT sequences can be searched together. The Office has not demonstrated that it would be a burden to examine all species of origin at the same time.

Applicants respectfully request that the Office reconsider the present restriction requirement, and rejoin all claims pertaining to TRT polynucleotides (Groups 7-12).

New claims 105-118 are supported in the specification. Support for the structural motifs of, e.g., claims 105 and 108, is replete in the specification. See, e.g., page 42-43, especially page 42, line 25 (referring to Figures 55 & 57) and Figure 55. Support for "vertebrate telomerase" is replete, see e.g., page 7 line 3. Description of increasing replicative capacity (as recited in claims 111-115) using telomerase is replete, see e.g., page 100-101 and original claim 44. SEQ ID NO:117 (new claim 114, 118) corresponds to human TRT cDNA (see, e.g., Fig. 58).

In view of these remarks, Applicants respectfully request entry and examination of new claims 105-118.

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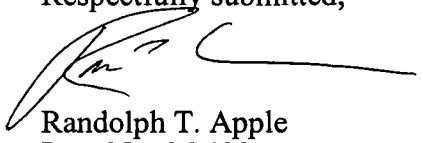
If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,



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